

Figure 1 Gregg, R.K., et. al.

91A ₃ H	_____ D _____	PHE ASP TYR TRP
TYR PHE CYS ALA ARG SER TYR TYR SER GLY ASP MET TYR CYS		TTT GAC TAC TGG
TAT TTC TGT GCA AGA TCG TAT TAC TCT GGT GAT ATG TAC TGC		
91A ₃ H-INSβ	_____ INSβ _____	
- - - - -	HIS LEU VAL GLU ALA LEU - LEU VAL CYS GLY ARG GLY - - -	
- - - - -	AGC C-C CTA GTG -AG -CG C-T --- CT- GTT TGC GGT GAA AGA GGT ---	
91A ₃ H-HEL	_____ HEL _____	
- - - - -	ALA MET LYS ARG HIS GLY LEU ASP ASN TYR ARG GLY TYR SER LEU - - -	
- - - - -	GCA ATG A-G CGC CAC -GG A-A G-- AA- TAT CGG GGA TAT AGC CTC ---	

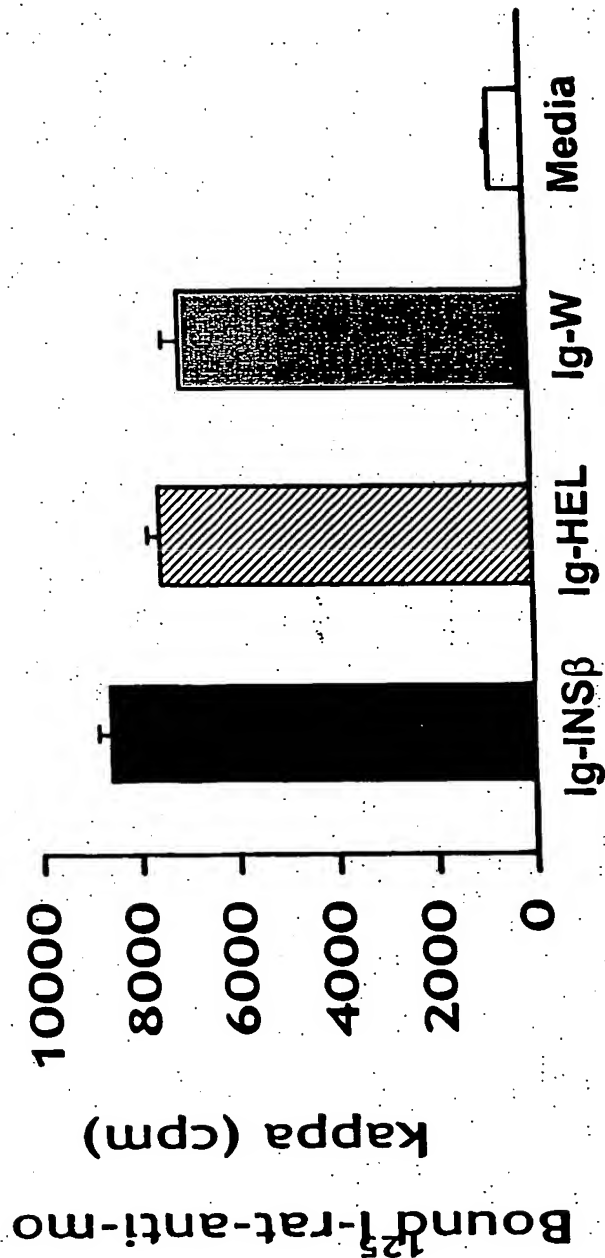


Figure 2 Gregg, R.K., et. al.

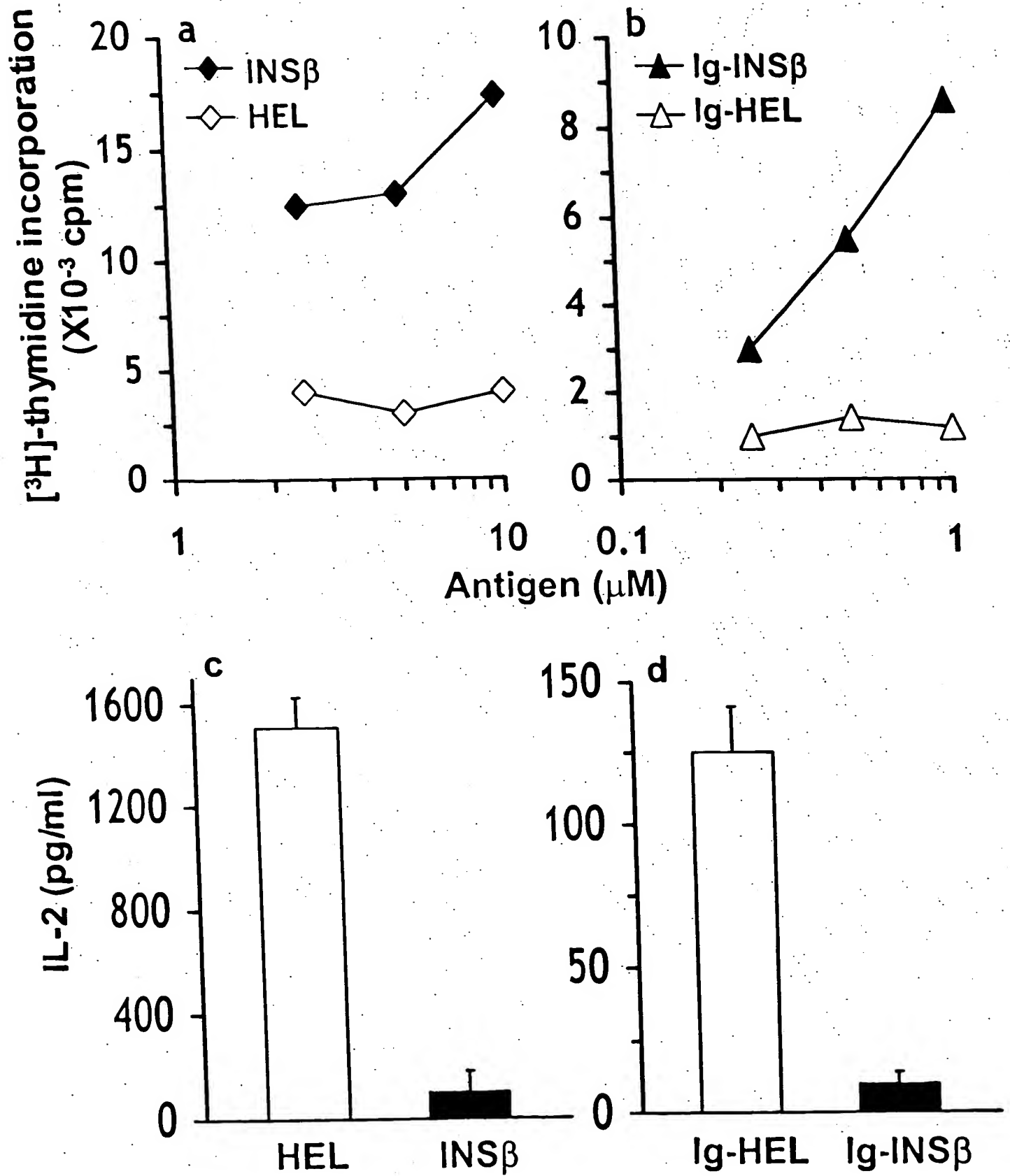


Figure 3 Gregg, R.K., *et. al.*

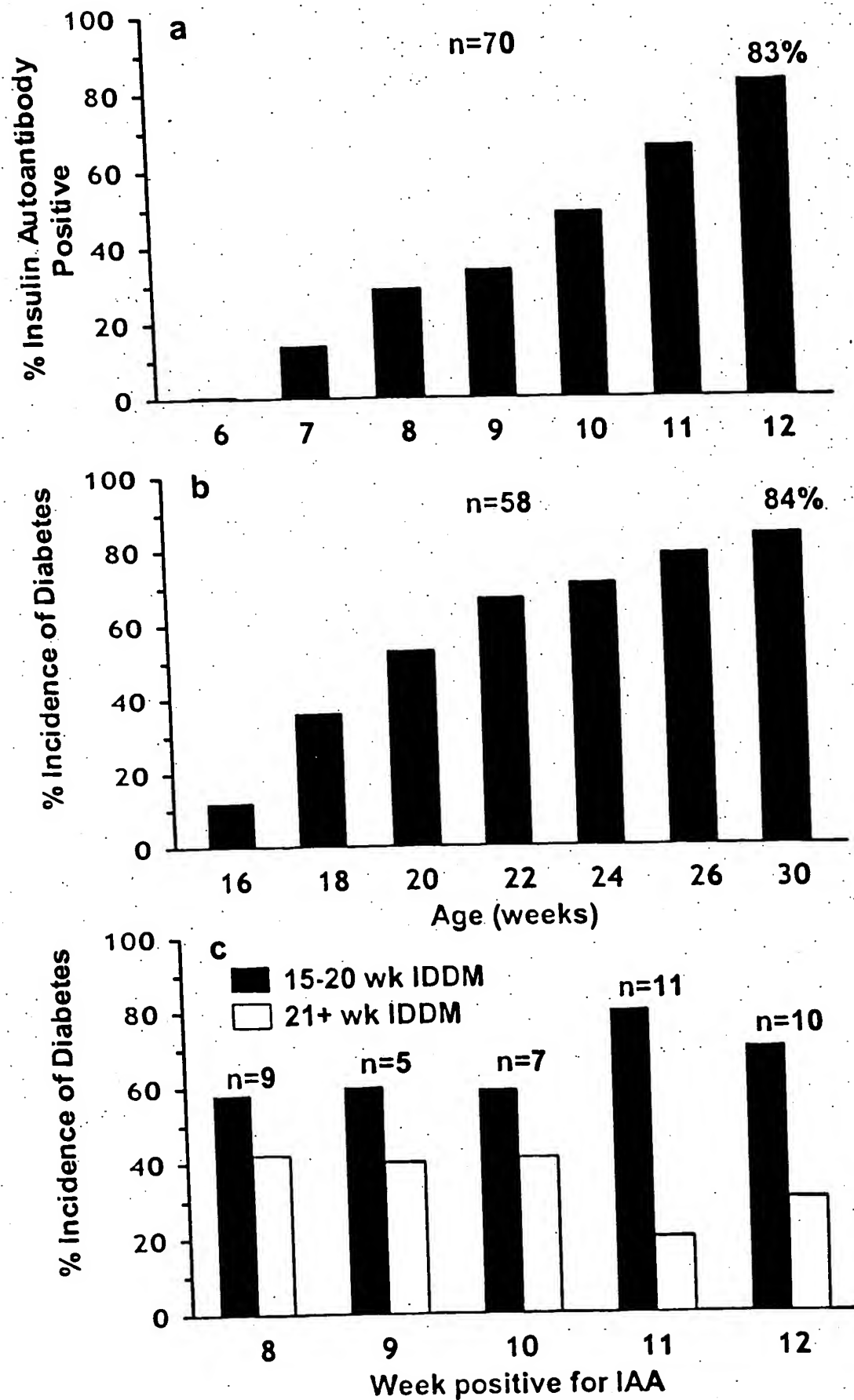


Figure 4 Gregg, R.K., et. al.

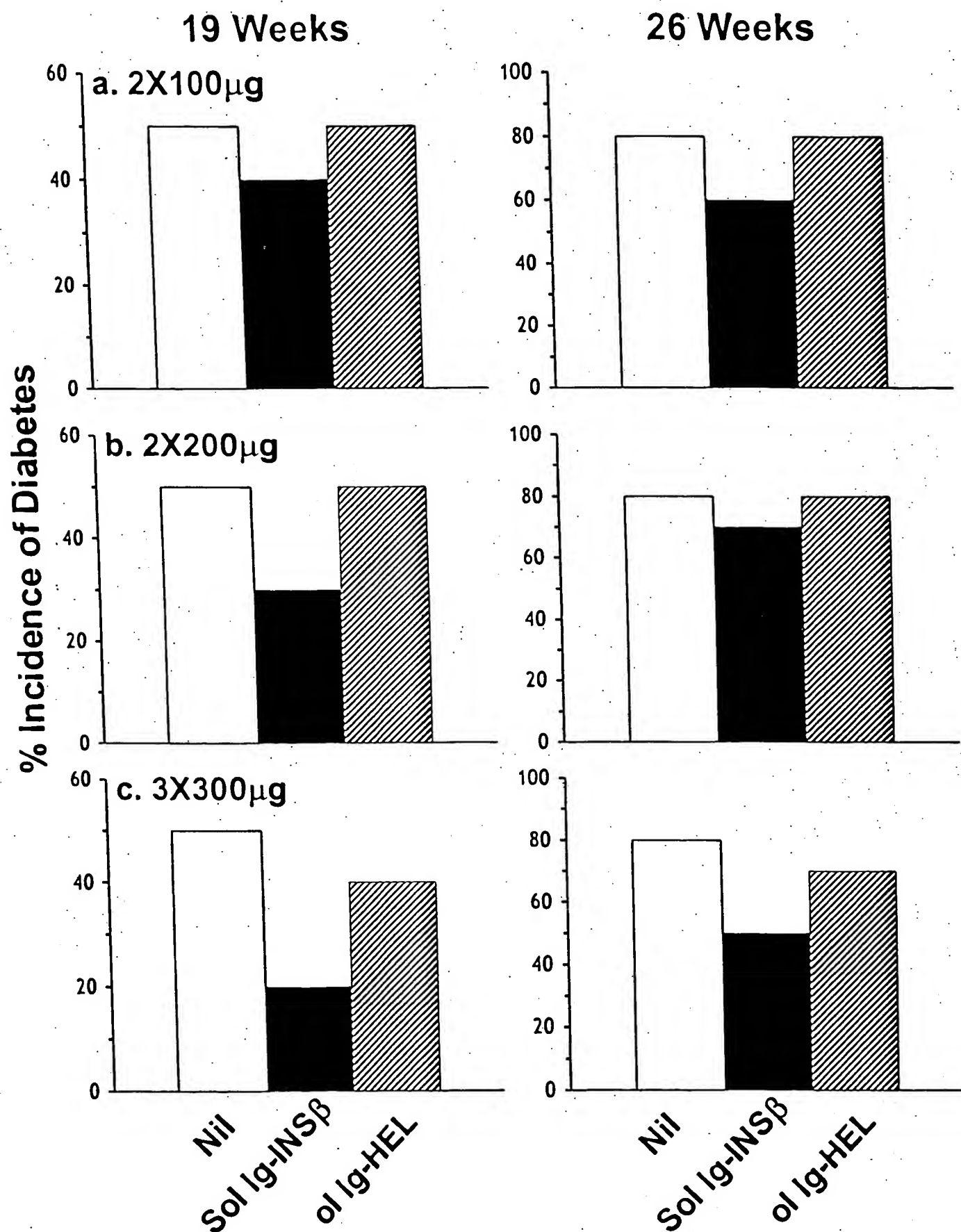


Figure 5 Gregg, R.K., et. al.

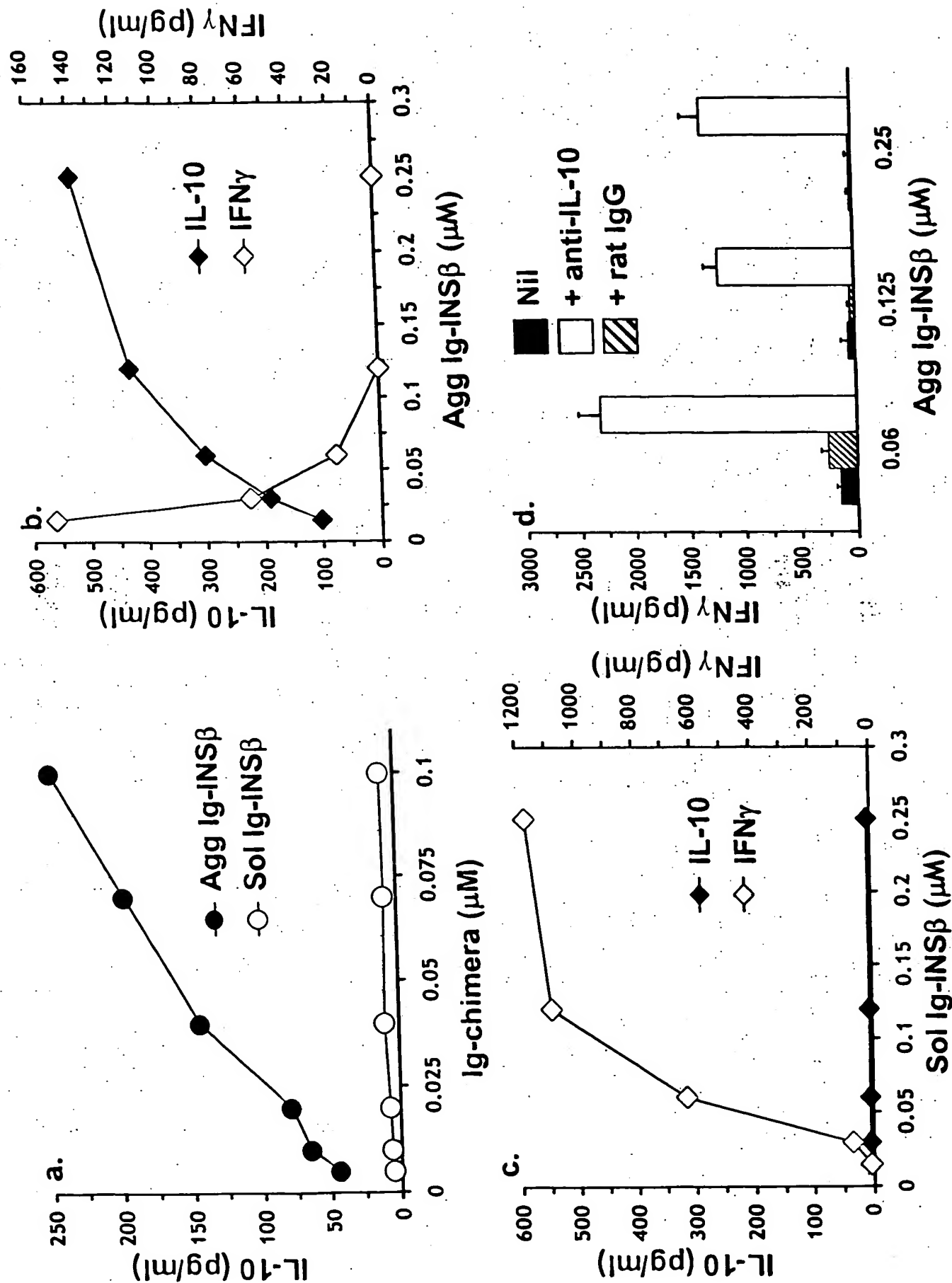


Figure 6 Gregg, R.K., et. al.

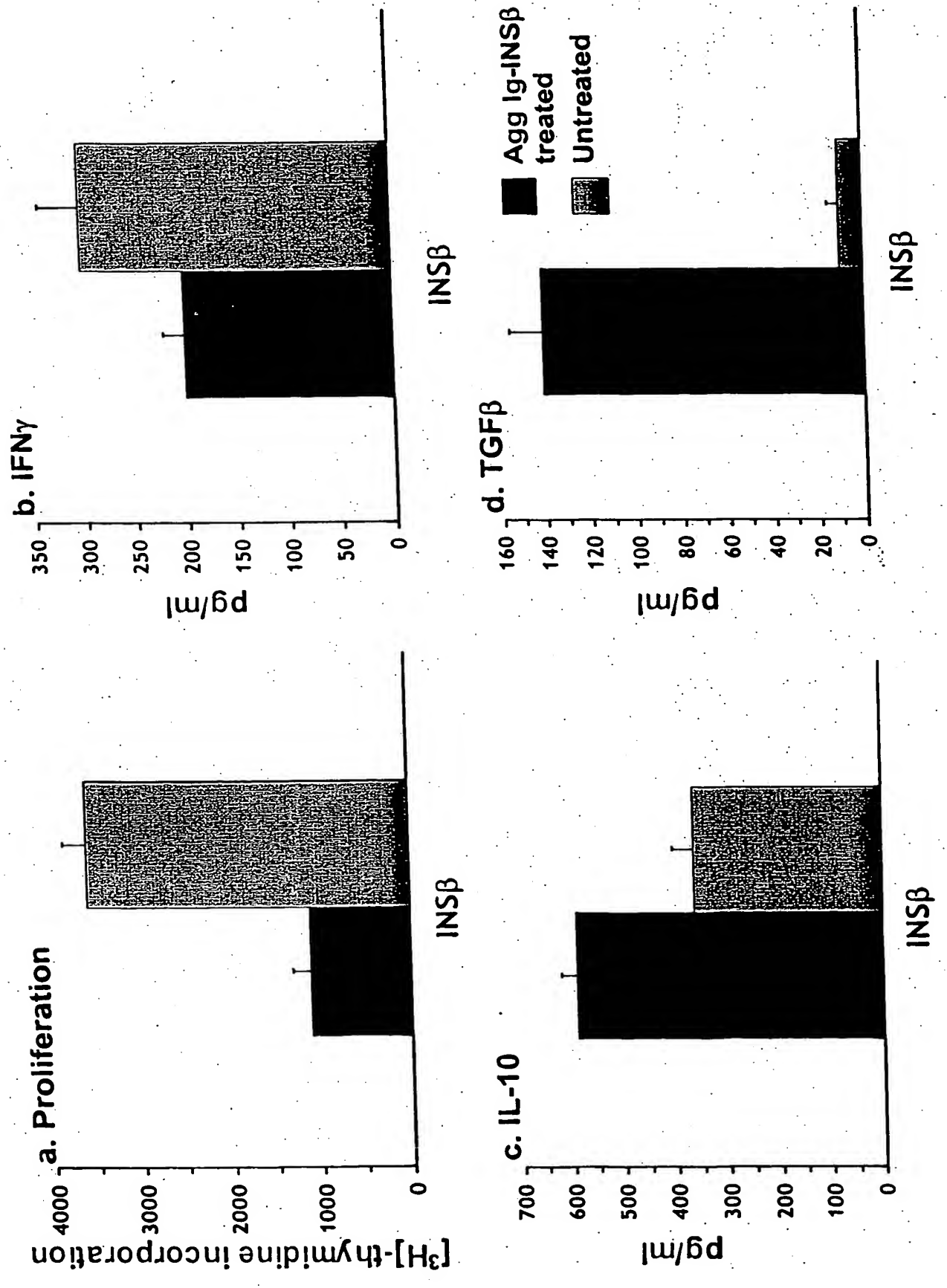


Figure 7 Gregg, R.K., et. al.

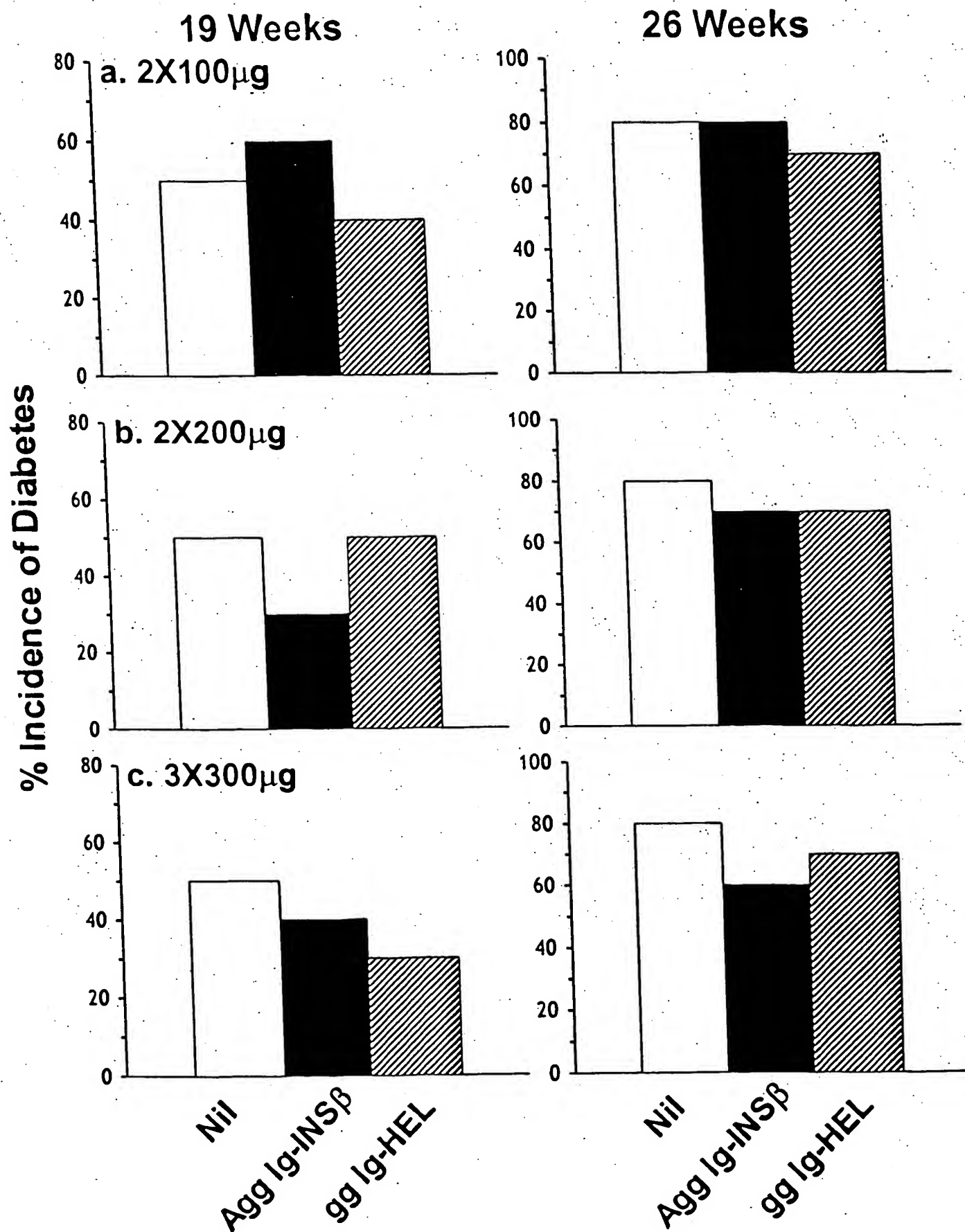
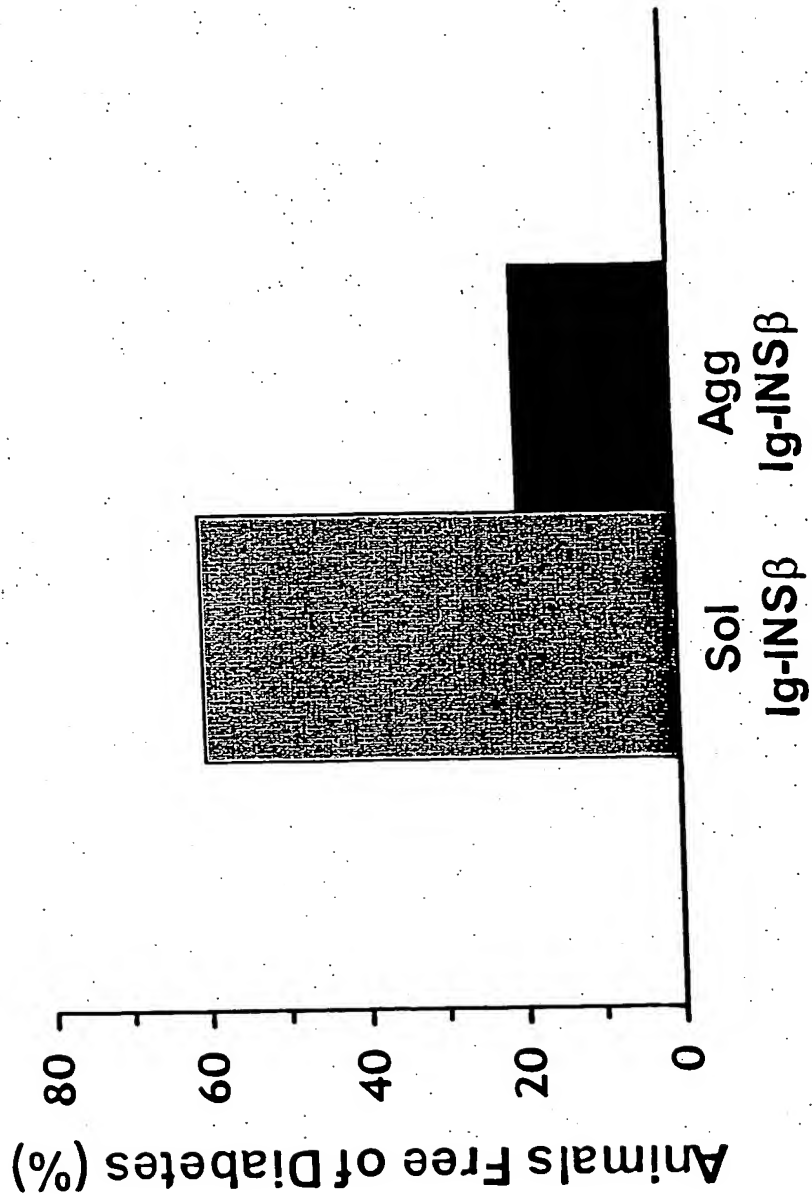


Figure 8 Gregg, R.K., et. al.



Figur 9 Gregg, R.K., et. al.

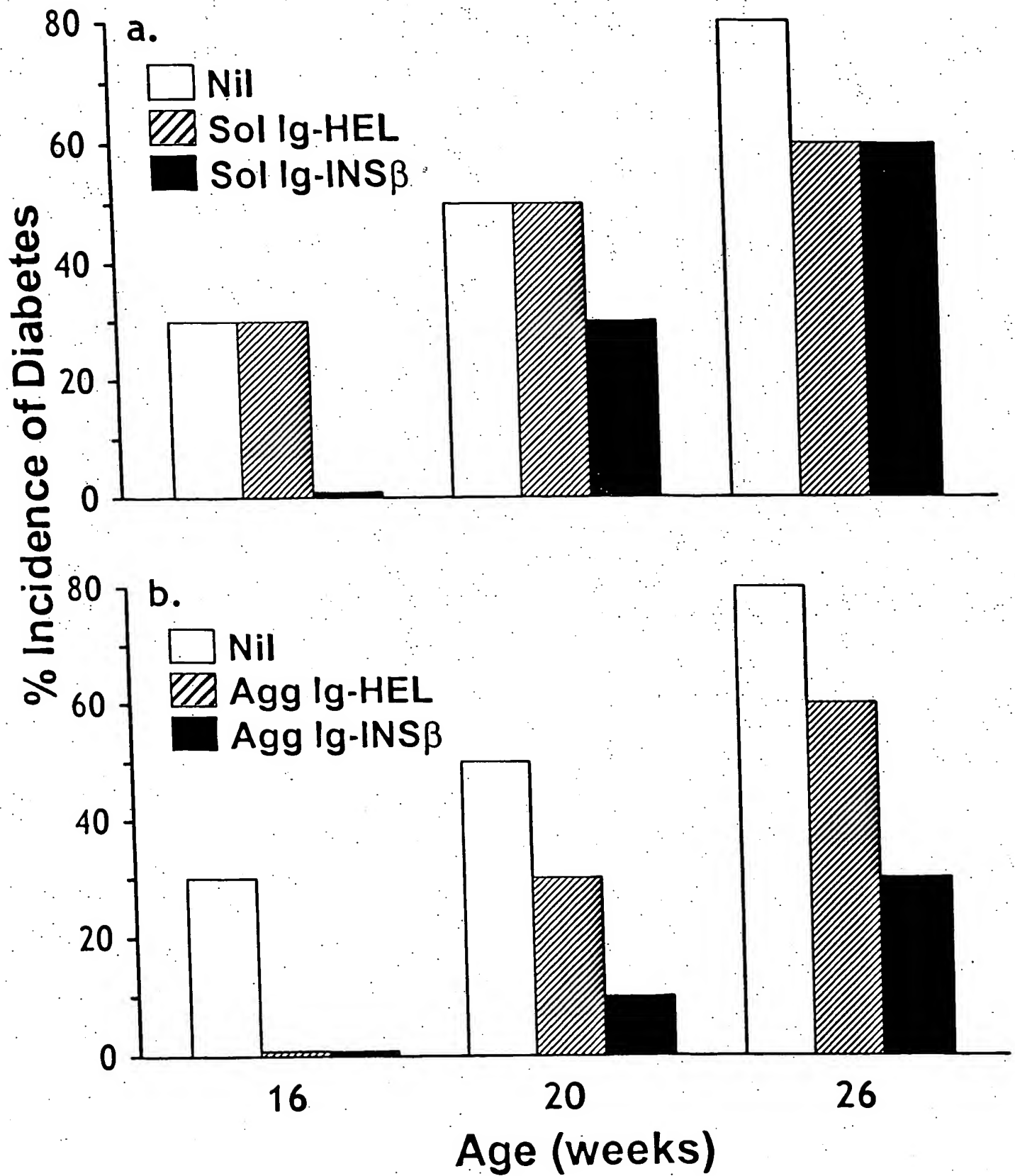


Figure 10 Gregg, R.K., et. al.

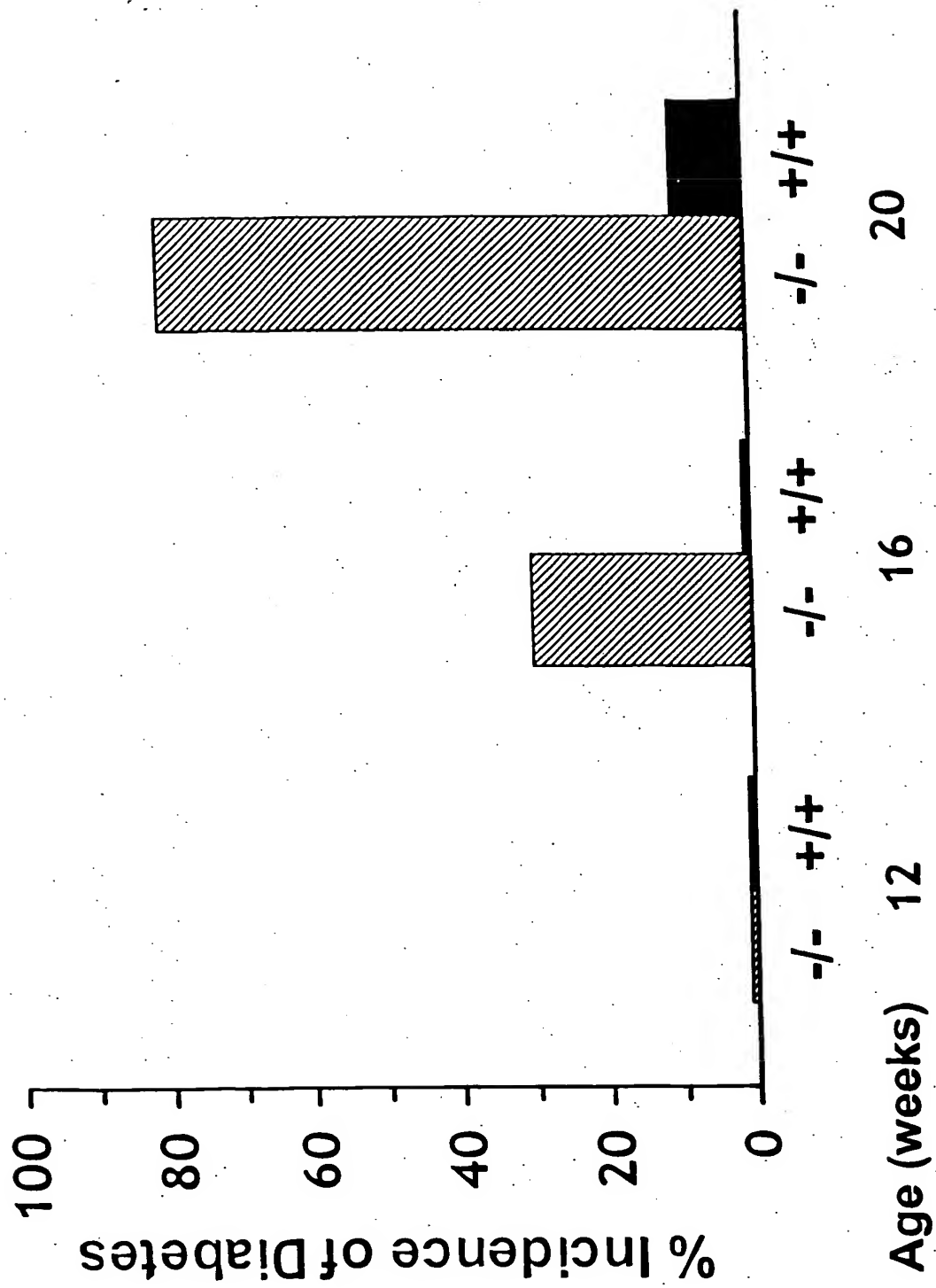
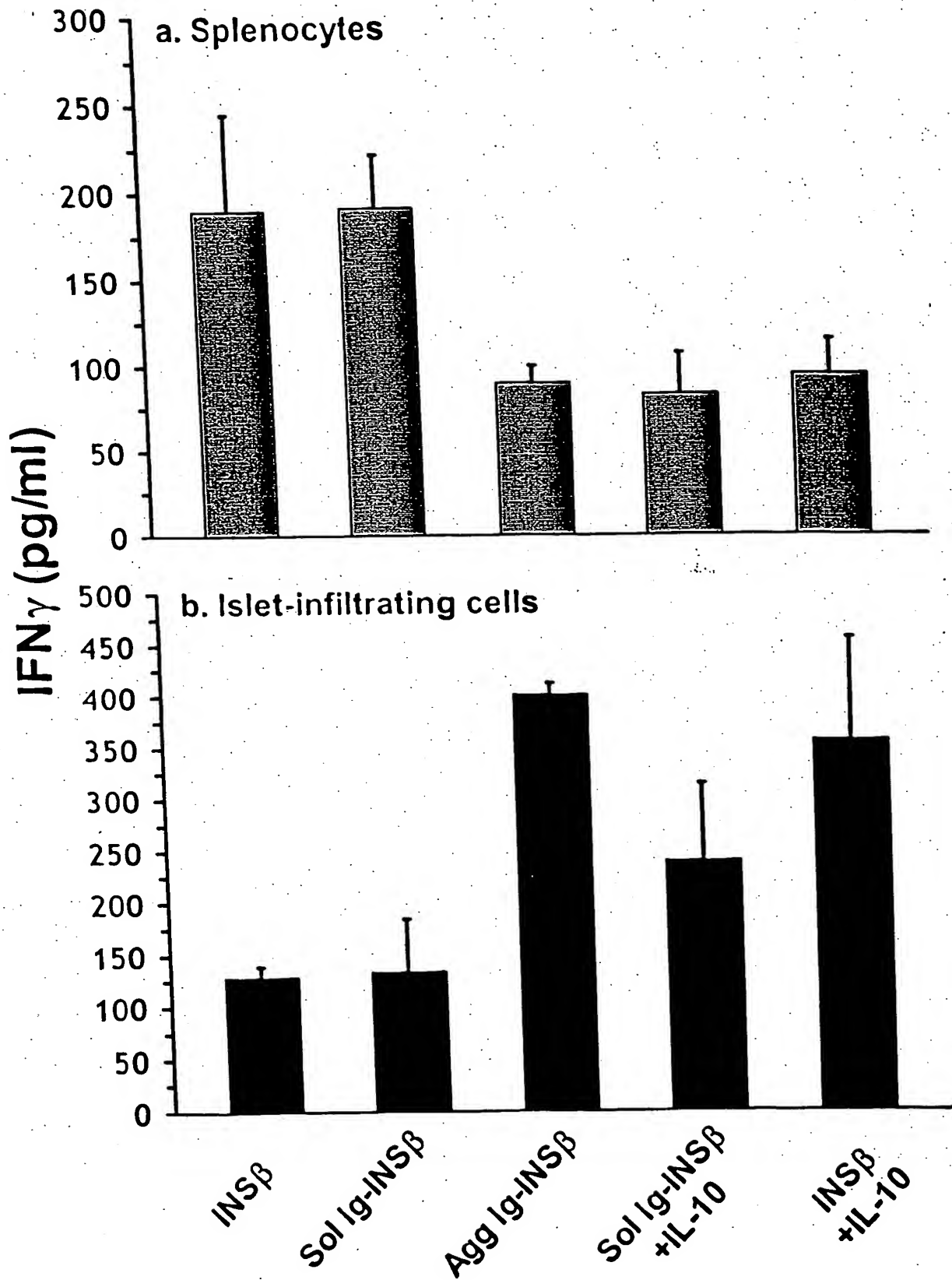


Figure 11 Gregg, R.K., et. al.



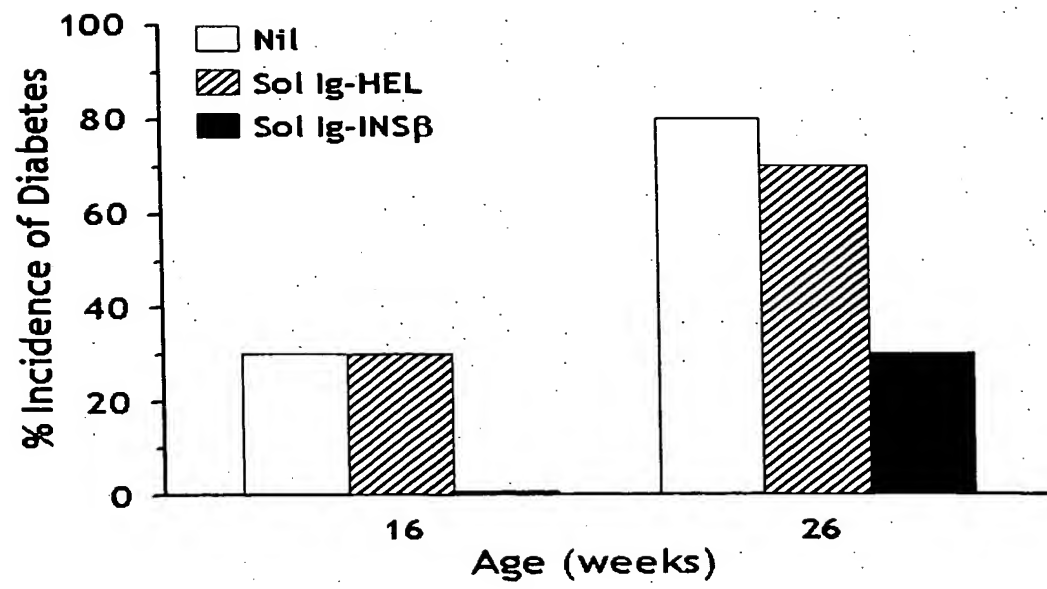


Fig. 12